

## FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGTTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCCTACCAAATGCAGCCCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTGAAATTTTCAACCACCTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGA  
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTCTGGATTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTTACCACCTTCAGCATCAGGAAGTGAAAATCTTACT  
CTTATTC AACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAAACAGCTGATCT  
ATATGTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT  
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTGGTCCCAACACATTTCTTCACTTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG  
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG  
ATGTGATCTTCCGTGGTCAGCGCTCTCTCTAGCATACTCTTCCCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACCAGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTCACCTTCATAGCATACTCCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTAAAGGTTACATGGAAAAGGTTATAGCTTTG  
CCTTGAGATTGACTCATTAATAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYPFWKMNLCVILLILVEMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFWFKLGGP  
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDALAEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTCKFFYAISSSKSSNVIVLLLAQIMGY  
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSAALSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
 AGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
 GTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTTCACAG  
 AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTTCATCTCTAG  
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGA  
 GCCGACAGTTTGAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
 ATTATCACCACCAAAGATCCCATTATCAACACTCAAACGCAACACAAACAGAATTTATTGT  
 CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCCTC  
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTATG  
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGA  
 AGCTGCTGGGTTTGGAGGTGTCCACCGGCTCTGCTAGTGCTTGCTCTCCTCTCTTTGGTGCTG  
 CAGCTGGTCTTGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAA  
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA  
 TGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC  
 GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTT  
 CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCA  
 CCCTTGGTTCTTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAT  
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCT  
 TTCTAGCCTGGCTATGTCTAATAATATCCCAGTGGGAGAAAGGAGTTTGGCAAAGTGAAGGAC  
 CTAACATCTCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG  
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT  
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA  
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC  
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
 AAAATAAAACTCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATCAACAAACATTTGCTGAATAGCTACTATATGTC  
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCTCAAAAAATTGCACATAGTAG  
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAAACTAAT  
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAT  
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC  
 ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAACTT

## **FIGURE 6**

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPPEESKSPSKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCCGGC  
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCCTGCTGTGCCCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCCGCCCCG  
GCTCTCAGCTACCCGCAAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT  
GGAGGACACGCAGCACAATTTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACCAGAC  
TGGACAAATGGTCTTTTCAGAGACGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG  
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTA  
CATCTTCTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTACAGT  
CCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGTTAAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG  
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAACATCAACCTGGCAAAAATG  
CAACAAATGAATTTCCACGCAGTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTGTC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTTCTTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTTCACAGTGTGGGGCAGCCGTCTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTGATGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCLTRDSECCGDQLCVWGH  
TKMATRGSNGTICDNQRDCQPLCCAFQRLFPVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCACCTTGTGAACCTCGTGGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTCTGGACCCTT  
AACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTACC  
ACACTGGGTCAATTGGCATTTGGAGCCCTCATCTGACCCTTGTGCAGATAGCCGGGTCACTCTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTCTGCTCGTGGACAAAGTACAGACCTGTGCTGTTCTTTGGGAAGCTGTGGT  
GGTCGGAGGCGTGGGGTCTGTCTTCTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCACCCTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAGATTTTATTAAAGATATTTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGFLFWTL  
NWVLALGQCVLÄAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

### **Important features:**

#### **Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### **N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

#### **Hypothetical YBR002c family proteins.**

amino acids 276-288

#### **Ammonium transporters proteins.**

amino acids 204-231

#### **N-myristoylation sites.**

amino acids 60-66, 78-84

#### **Amidation site.**

amino acids 306-310

## FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCTCTTCTTCTGGGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCGGGCGTGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGAGGGGGCC  
GGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG  
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA  
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC  
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCAACATCTGGTCTACTTCGGCGTCGTGGG  
CTCCTTCTCTTTCATCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGTGCCCTGGTACGAGGCCCTCTTCTTCTTCACTCTCCTC  
TTTACTTGCTGTCGATCGCGGCGTGCGCTGATGTTTATGTACTACTGAGCCAGCGGCTGCCA  
CGAGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGCTCATCGCTGCTGTCTCTGC  
CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCTCTACACCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG  
TGGGCCTCATCATCTTCTCTCTGTGCACCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC  
ACTTCTGCCTGGTGCTGGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG  
ACCCGGAAGATGATCAGCACGTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT  
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC  
CCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGGC  
CTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCTCTTCTCTTCCCTCCTCCTGTGCCCATACTCAGCATCTCGGATGAA  
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGCTGCTGGAGAGAGCGGGGAACCTCCACCACAG  
TGGGGCATCCGCGACTGAAGCCCTGGTGTCTCTGCTCACGTCCCCAGGGGACCTGCCCCCTTCTCTG  
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

## **FIGURE 12**

MGACLGACSLSCASCCLGSAPCILCSCCPASRNSTVSRLIFTFFFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSIMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444



## FIGURE 13

CGGGCCAGCCTGGGGCGGCCGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
GGTTGGA AAAAGACTCCTGTAACCCCTCCTCCAGGATGAACACCTGCCAGAAGACATGGAGAACG  
CTCTCACC GGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG  
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTCATTTCATC  
CTTGCCCTGGATTGAGACGTGGTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTCAATTCAC  
AGAATGGAATTTTTTGTTCATGTCTCAGATTTATTTTGATTTCTTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQAGFYVLPIISFILAWIETWFLDFKVLFPQEAEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCCCTGCCCCGCCCCGCTCCCTGCGCCGCCCGCCCTCCCGGGACAGAAGATGTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCTGCCCAT  
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCCGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCCTGACG  
 CGCCTGCGGCTGGCCGGCAACCCGCTTGGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGGTTTGGCCCCCTGGGTGCGGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCA  
 CTTCCCGCCCAAGAAGCCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG  
 CCACCACCAACACAGCCACAGTGCCCAACACAGAGGCCGCTGGTGCGGGAGCCACAGCCTTGTCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCGCCCTC  
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACG  
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG  
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA  
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGGGCCGGGCGGGTGCCGGAGG  
 GCGAGGAGGCTGCGGGGAGGCCCATACACCCAGCCGTCCACTCCAACACGCCCCAGTCACC  
 CAGGCCCGCAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCCTTGGAG  
 CCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCAGTGCCATGAGGACAGTGTCGCCCTGCCCTCCGCAACGTGCAGTC  
 CTTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCAAGGAACAAAAGAACTGGAAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAAAATATATATATTTATAAGAGATCCTTTCCATTATTCT  
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAA  
 GGCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDVPPDTPVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDTANVE  
ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQGRPSPTP  
VTPRPPRSLTGIEPVSPTSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCMPLGPRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAAQDKGVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPIMGFPGLQSPHAKPYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 579-599

#### **EGF-like domain cysteine pattern signature.**

amino acids 430-442

#### **Leucine zipper pattern.**

amino acids 197-219, 269-291

#### **N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

#### **Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

#### **N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## FIGURE 17

GCAGCGGCGAGGCGGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTCAGAAGAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG  
AAGATATCAGCTTTCTAGAGTCTCCAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA  
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG  
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAAATCCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTTGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT  
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTTAGTGGAAGGCT  
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTCATGATC  
CAGATTTGCTTGTATTAAGACCAAATATTCAAGTTGAACCTCCTTCAAATCTTGTAAATGGATAT  
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG  
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG  
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA  
AAATTTTGTAATGGTGGCTATAGAAAACAACATGAAATATTATACAATATTTTGCAACAATGC  
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAAAGTCCAGAGAGCTCTACTTTCTG  
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG  
AAGATTAACCTATTTTAAATAAAATTATGTCTAAGATTAATAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEP KVRKPALTAIEGTAHGEPCHPFLFLDK  
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLI AHMVLVSRL

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

#### **Tyrosine kinase phosphorylation site.**

amino acids 220-228

#### **N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

#### **Glycosaminoglycan attachment site.**

amino acids 267-271

#### **Microbodies C-terminal targeting signal.**

amino acids 299-303

#### **Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

#### **Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCCATCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT  
AAAAAGGGATTTTATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
AACCTCAGAGAGACTTCGTAAGTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGTCTCTGGGGTCTGATCAATAATGCTGGTGT  
CCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAACAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCCAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCT  
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA  
TCTTTACCGTGGCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTNLMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGENDSLRRDMK  
AFGVHVSCLIEPGLFKNLADPVKIVIEKKLAIWEQLSPDIKQOYGEGYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



## FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTTATACAATTGA  
CATTAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAGGAGCATTT  
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT  
GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTGAGGAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGA  
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTT  
ATGTCTTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC  
TGTTTGAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAACATCA  
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
GAGACCATGTCTATTAAAAATATAATGGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA  
GAAATTTATATGAAAATTTATCTGAGTCATTAAAAATCTCCTTAAGTGATACTTTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYITIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDDVDNLT  
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 75-79, 322-326

#### **N-myristoylation site.**

amino acids 184-154

#### **Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAAGCCCGCCCGCCGCCACACCCCTCTGCGGTCCCGCGCGGCCTGCCACCCTTCCCTCCTTCCCC  
GCGTCCCGCCTCGCCGGCCAGTCAGCTTGCCGGGTTCGCTGCCCCGCAAACCCCGAGGTACCCAGCCCGCGCCTCT  
GCTTCCCTGGGCCGCGCGCCCTCCAGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCAGGGACCGTTGCCTGA  
CGCGAGGCCAGCTCTACTTTTCGCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCC  
TCCAGCTCCACTCGTAGTCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAAA  
GGTGGGAACGCTCCGCCCGGCCCGCACCATGGCACGGTTGGCTTGCCCGCGCTTCTCTGCACCTTGGCAGTGCTC  
AGCGCGCGCTGCTGGGTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGCTCTTTACGTGTCAAAGGCTTC  
AACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTG  
CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATCTTCAAAGAAGTACTTTGAAAATGCAGAGAATCCCTG  
AATGATATGTTTGGAAGACATATGGCCATTTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG  
TTCCGCCTGGTGAAGTCCAGTACCATTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTCGGAGATGTCCTTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGCTCAAGGC  
TTAGCGGTTCGGGAGATGTCGTGAGCAAGGCTCTCCGTGGTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAACATCATGAGAGGC  
TGTTTGCCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGAGAGAGGCTA  
GAGGCTCCTTTCAACATTGAATCGGTGATGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT  
AATAGTGTTCAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCAAGCCCTCCAGCTGGAGGAATTTCTCGT  
TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACT  
AGTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCTCCCTTCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC  
CTGTTTGCAAGTACAGGAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAAACAGAC  
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGCTCCTGGGGCA  
CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTCTGGTTATGCAGAGAGTGGAGATTAATTCTCAAACCTCTGAG  
AAAAAGTGTTCATCAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA  
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTATTCAGTTTTGGG  
AGGAAAAGGGACTGTGCAATTGAGTTGGTTCCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCAATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTTCTCATTTCTGTTTGGGTT  
TTTTTTTCCAACGTGATCTCGCCTGTTTCTTACAAGCAAAACAGGGTCCCTTCTGGCACGTAAACATGTACGTATT  
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH  
LYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVVNPTAQCTHALLKMIYCSHCRGL  
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEVQVDT  
KPDILILRQIMALRVMTSKMKNAYNNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

#### **N-glycosylation site.**

amino acids 514-518

#### **Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

#### **N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

#### **Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCCTGAG  
AGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISL L L L L L P I M L M S M V S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K F M  
T V S G L P K K Q C P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

## FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC  
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCCGAACCGGAGC  
CAACTTTTCACTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACCCAAATCCCCACTTTGAGA  
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG  
CTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTCT  
GAGCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA  
GCAGAATGAGAGAAGACATTCACTGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC  
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC  
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCVSVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFSSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207



## **FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG  
CCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

## FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGG  
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC  
TTCAGATTTCATCACCACCCTTCTGGTTTCACATTTTCATTTCATTGGTTATTTTGGGATTGTTGTT  
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGAATATAAGCCCCCTTCGGGCATTTCGGTACATGTGGTCGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAG  
TGGTTACTTGTATTTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC  
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG  
GATTCCGAGAATCATTGTATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAGATGC  
ATTCAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC  
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
TTAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE  
LDTERENMKCVLGFIAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTF  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNPDHPILSSLSILFFYHQGT VVKGSFLISVVRIPRIIVMYMQNALKEQQHG  
ALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLV AHSFSLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

## FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTTAGA  
 ATAAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCTGTGTGGT  
 GAAAATTTTTTAAAAAAAATTCCTTCTCAACAAGGGTGTCTTCTGATATTTATGAGGAC  
 TGTGTTCTCTACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGTGGTGAAGTGGAGTAC  
 ATTCAAACAAAGAAACGGCAAGAAGATTAAAGGCCCAAGTTCACTGTGCCTCAGATCAACTGC  
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTTATTGTGAAATGTCCAGCAGGATGCCAAGA  
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG  
 TACACAGTGGTGTGCTTGATAATTGAGGAGGAAAAATCTTGTTCGGAAGGTTGCTGGACAGTCT  
 GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT  
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT  
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG  
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
 CACCTTGCCAAGGCCATCCCTTCTGCTGCTTCTACCACCAGCATCCCAGACCACAATCAGTGG  
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAAACAGGCC  
 AGAGCTGATCCAGGTATCCAAAGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC  
 GGATGTCAGCCTGGGACTTGTTCAAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCC  
 TGGGAGATCCAACTGCAAAATTGACTTGTGCTTTTTTAATTGATGGGAGCACCAGCATTTGCCAAA  
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGTC  
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC  
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT  
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAATCTTTTTCCAAAGCCAATGGAAACAGAAGCGG  
 GGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTTCAA  
 GACTTGCAGAGAGTCAGGAATCAACATTTTCTCATCACCATGAAGGTGCTGCTGAAAATGAG  
 AAGCATGATGTGGTGGAGCCCACTTTGCAACAAGGCCGTGTGCAGAACAACCGCTTCTACTC  
 GCTCCAGCTGCAGAGCTGGTTTGGCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGGTCTGCG  
 ACACTGACCGCTGGCTGCAGCAAGACCTGCTTGAAGTGGCTGACATTGGCTTCGTATCGAC  
 GGCTCCAGCAGTGTGGGACGGGCACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCAA  
 AGAGTTTGTGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC  
 TGGAGTTTGGGTTCCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC  
 TACTGGAGTGGTGGCACCAGCAGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCGACGGGAGGTCTACGACGACGTCC  
 GGATCCCAGCCATGGCTGCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCCTGGGCT  
 GCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCACTCCTTTTGTGGACGA  
 GTTTGACAACCTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC  
 AGCCTCGGAATGCAATTCAGAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT  
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC  
 AAATGTCTTGTATTATTCTTTGCCATCATGCTTTTTTCATATTCCAAAACCTGGAGTTACAAAGA  
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT  
 TTTGACAATTGTTTTCAAATAAATGTTGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG  
 AGCTTTTGTGAGATTTTAAAGTTGTTATTCTGATTGAACTCTGTAACCTCAGCAAGTTTCAT  
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNSGVQSLSLPRWR  
ESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMLLAVTVAVA  
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHTNLKTHNTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLLQPLVKRVCDDTLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALQQL  
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAWAAQEELEVIATHPARHDSFF  
VDEFDNLHQYVPRIIQNICTEFNSQPRN

### Important features:

#### Signal peptide:

amino acids 1-26

#### Transmembrane domain:

amino acids 181-200

#### N-glycosylation sites.

amino acids 390-394, 520-524

#### N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### Amidation site.

amino acids 304-308

[illegible][illegible]

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 20-39

#### **N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

#### **Glycosaminoglycan attachment site.**

amino acids 239-243

#### **Ly-6 / u-PAR domain proteins.**

amino acids 23-37

#### **N-myristoylation site.**

amino acids 271-277



## FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC  
TCGTCTTTCGCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGTGTG  
AATATGATCAGATTGAGTGCCTCTGCCCCGGAAGAGGGAAGTCGTGGGTTATACCATCCCTTGTGTCAGGAATGAGGAGAA  
TGAGTGTGACTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAATGGCTCATGGGGGGGT  
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCCATGTG  
GCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGC  
TAAACCTGGGTTTGTATCCAACTAAGATTTGTGATGTTGAGTCTGGAGTTTGGACTACATGTGCCAGTATGACTATGTTGAG  
GTTCTGTATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTTGTTCATGACGGCAGCTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGGCCAGTCAATGGGTACCAGAAAA  
TAACAGGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATGGCACCGTGGTGTCTTCTTTTGTAACTCCATATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCGATGCAGGTTTCAAGGGAGACACCATACACCACTAT  
ACTCAGCGGCCCTTCAGCAAGCAGAACTGCAGAGTGCCCTTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCGCCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGATCTCACCCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCCTGCATCCTATCTGCGGGAAAAATGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCAGGCGGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACAAAGGGAGC  
GTGGTTCTTAGTCTGCGAGCGGTGCCCTGGTGAATGAGCGCATGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTCACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTTCTGCTATCATTCTGCATCCCACTATGACCCCATCTGCTTGTATGCTGACATCGCCATCCTGAAGCT  
CCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAGTGGGATCTCAGCACTTCTTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG  
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGATGCTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATGCAGAGACAGGAGGCATCGCGGCTGTGTCCTTCCCGGGA  
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTTACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCTGTGAAGTGGCT  
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG  
GCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCT  
GAACTACAAAAA  
AAAAA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAACHCVTDLGKVTMIKTADL  
KVVLGKFYRDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLFPKDWI  
ERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC  
TGGTCTTGCCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATTGAGAACTCTGTA  
AAGGTGCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCAGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCTGGCCTAGACA  
ACCTTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA  
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA  
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGAAAAATTCTGAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGA  
GCAGGAACAATGGACAGGCCCGGATGCCACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGGAAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCCAGAAAGTGGCGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTCACTCGTGTCCCGCCAGGTTGGGCAGC  
GGAGCCCTGACATCTTTGAGGAAGCCGGTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACA  
CTCCCAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG  
GCATGACCGTCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATGATTGAGCCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAAGTGCAGAGGTGAGCC  
GGAGTGAGGAGTGGCATTATTGAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCCAGTGAAGTGGTCCCCATCCT  
GGGTGATGTGGCTGGAATTACCACGGTGTGTATAACTGTAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAAGTTAAAGGAAGATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGAATCAATGATGGGTGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC  
TTGTGAGTTTTATATTTAAAGAAAGAAATACATTGTAATAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCAAAAAATTAAGTACTAGTTTTTTTTCAGTGTGGAGATTCTCATTACTCTAC  
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAACTAAATGATTGATTGTATACCCCACTGAATT  
CAAGCTGATTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCT  
AAAAATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATTTTTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDIFQEAGWNSNGSWSPG  
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTG DILLNV DGV ELTEVSRSEAVALLKRTSSSIVLKALEVKEYEQEDCSSPAALDSNHNMAPF  
SDWSPSWVMWLELPRCLYNCKDIVLRRTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC  
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCC  
ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
GACAACGTCTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
CTTTACAGAGGGTCGCCATCTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTTCTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCTACCTCACCAGGCTGAAGG  
TAAAAAGTTTAAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTG  
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTGTCTTTATAAAT  
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC  
TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTCT  
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT  
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGCGCTGCAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCCTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

## **FIGURE 42**

MGENLTFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTTALSREQFFKVNGFSNNYWGWWGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG  
ACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC  
TTCCTTATTTATTCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT  
TCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12



## FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTCCACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTGAGCAGAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG  
AAACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCCTTCAA  
CTTGCACTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCTGTTGGGCT  
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHRLIHFSVFLGL  
LLVGILEVLFLGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA  
CATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACATCACTCCAGGCTCTGCCA  
CTACTTGCTAGGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPILITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
GTGCTTGGCCACAGTGGTGTCTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG  
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
CCTCCTGGGGATCCAGCACC GGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
CATAAACC CGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGG  
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTG  
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCTCCTTAA  
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGV  
GHSGAWETSGGHGIFGSQGGGLGGQGNPGLGTPVWHGYPGNSAGSFGMNPQGAPWGGGNGGPPNF  
GTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS  
SSGSSSSGSSSGSSSGSSSGSSGSGSGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE  
ARGSGESGIQGFRRQGVSSNMREISKEGNRLLGSGSDNYRGQSSWGSGGGDAVGGVNTVNTSETSPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

### **Signal peptide:**

amino acids 1-21

### **N-glycosylation site.**

amino acids 265-269

### **Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### **Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### **N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

### **Cell attachment sequence.**

amino acids 301-304



## FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCC  
CACAGCCCCCAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT  
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGCCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTCCGCA  
GGGCCCAGGAACATGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCCTGGCGTTGAT  
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGACAGTGA<sup>ACTTTCTGAC</sup>  
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFQPQPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPFIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEIGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFDDAVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

### **Important features:**

#### **Transmembrane domains:**

amino acids 13-32 (type II), 77-102

#### **Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

#### **N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCGGTGTGTCTTGC  
ATAATTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT  
GTGATTGGAACATTTGAGGGTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTCAGCAACAGCAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

10063527

## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG  
TACGTGCCGGTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTATCCCCCTCCAGGAATTTCCACCTACCGCCAGTGGAGCAGAAAATGTACAAGCT  
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCGAGAAAAAATTTCAAGAGCATGGATAAAAACGGCAGCATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACCTCTCCACCCCGTGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCGACGCGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGGCCAGG  
TCACTCTGGCGGGGCAATGGCATCAACGTCCTCAAATTTGCCCCGAAATCAGCCATCAAATTCATGGCCTATGAGCAG  
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTCAGAGAGGCTTGTGGCAGGGTCTTGGCAGGGGCC  
ATCGCCCAGAGCAGCATCTACCCAAATGGAGGTCCCTGAAGACCCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA  
ATGCTGGACTGCCCCAGGAGGATCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG  
GGCATCATCCCCATGCCGGCATCGACCTTGCACTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTG  
AACAGCGCGGACCCCGGCGTGTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAACATATCTGCGGACCGAGGGGGCCTTGGGCTGTACAGGGGGCTGGCCCCAACTTCAAGGTTCATCCCA  
GCTGTGAGCATCAGCTACGTGGTCTACAGAACCTGAAGATCACCTGGGCGTGCAGTCCGGTGCAGGGGGAGGGC  
CGCCCCGCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACCT  
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCAACCCGAGGGAGGGTGGGGAGAGCTGGCAGGCCCAGGGCTT  
GTCTGTGACCCAGCAGACCTCTGTTGGTTCAGCGAAGACCACAGGCATTCCTTAGGGTCCAGGGTCAGCAGG  
CTCCGGGCTCACATGTGTAAAGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT  
TAGTCTTCCATTTACCCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC  
CCTCTTGCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGC  
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCCTGGACCTGTGAGGATGGGGCCACCTCAGAACCAACTCACTGTCCCCTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTGGGGCGAAGGGCAGAGCGTTTGTGTCTGGGGAGGGAAGGAAAGGTGTTGGAGGCCTTAATTATGG  
ACTGTTGGGAAAAGGTTTGTCCAGAAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAACCCAGCAGGGGCGCAGC  
GGGACCAAGCCCACTTCCACTTGTGTCACTGCTTGAACCTATTTATTTTGTATTATTGAAACAGATTATGTCCT  
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCAATTTCAAGTTCAATTTTATTATTTATTTATGTTTATGTT  
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCCGCTGCAGTCACATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGCAGCAGCCCTGGCTCCTTTCCTTGGCAG  
GTTGGGGAAAGGCTTGGCCCCAGCCTTAGGATTTCAAGGTTTGAAGTGGGGCTGGAGAGAGAGGAGGAACTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCG  
TGAGGTGCCCTCACTGTGAATTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCCTCCAGC  
CTTCTGCTGCCCTTGTCTTAAATGCGGGCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAAATGACCTGA  
TGAGGAAATCTTCAATAGGATGCAAAGATCAATGCAAAAATGTTATATATGAACATATACTGGAGTCGTCAAAAA  
CAAATTAAGAAAGAAATGGAGCTTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG  
QLDFEEFVHYLQDHEKKLRLVFKILDKNKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWRRHLVAGGG  
AGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK  
FMAYEQIKRLVGSQDETLEIRLHVAGSLAGIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation sites.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGTGCTGATCAAGTGATAGTT  
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCAGGTGTGAGGCTCCCCGATGGTTCCCC  
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGTTGTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAAATAAT  
GTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTGATGTGAAGTAGACAAGTGTGTTAAGA  
GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 60**

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASL  
CVSSFFFAISWALLPLSPYMLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 258-281

#### **N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

#### **N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194



## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCTGGTGGTGGTTATGGGGGTCTGCCCCTGGAGGGCCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCCAGGAGGACCATATG  
GCGGTGCAGCTCCCGGGGGCCCCATGGTTCAGCCACCTCCAAGTTCTTACGGTGGCCAGCAGCCT  
GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCAGTTCAACCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATTGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGATTCTGCCACACCATAAAT  
CCTTGTTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAAATTTGCATTTTTTTTC  
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDEFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

## FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA  
AGCGCTGCCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTCTAATCACTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCGCTGATCACCCCTGGGGTACCCTGAATCCAGTG  
TGTCTGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCTCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC  
CCTCCTGGCTCTTCTTGGAAATCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVLCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPFAGGSQVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRNSLGGAGKILSQRP  
PWSLIHRVLPDHPWGTINPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGPLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC  
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLRLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVES  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 56-80

#### **N-glycosylation site.**

amino acids 36-40

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

#### **Tyrosine kinase phosphorylation site.**

amino acids 86-94

#### **N-myristoylation sites.**

amino acids 7-13, 26-32



## FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTGAGAGGTTTGTGTTTCTCTTAGTCTGTGCCTGCTGCCAG  
TCAAATACTTCCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTCCAGAA  
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
TTTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAGGCCAAAACATGAA  
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA  
GAATGTGGAGAGAAAGGCCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTC  
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT  
CAAGGAGGCAGCTGTCTTAGTAGCATGCAGAAATGATTCTACAACAAAACGTATGGAAAAGATTGTCAATTCTTT  
CCTGATAAAGTACAAACAGAAAAGCATCCATAATGTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA  
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAACATAAAGTGCAATTTTGAAGTACATGGGAGGTGATTAGCAAT  
TCTGAGGATTTTAAAAACACCATAACCATGGTGACACCACCTCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA  
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAGGACCGCCTAAATCGAATGAATCAAGCAGCA  
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACCTTGTAGTACTGCCACTATTGTA  
AATAGCTTAATCCAATAAAAGCAGTGATGAAGAAACACACTCATGGCAGGATTACCTACATATCTCTGGGAGGA  
ACTTCCATCTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATCCCAACTCGATGGATCCGAAGTA  
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGTATTGATGAAGTGAACAAAAGTGGGGCCATTGTTTCA  
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCAATTTTATGTT  
TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACATGATCTCTCCAGAA  
TCCCTTTCAGCTCGAAAGTAAGGGATTAAACACTGAATAGTAATGCCTGGATGAACGACACTGTCAATAATTGATAGTACA  
GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCTCCAGTATTTCTCTCTGGGATCCAGTGGAAACA  
ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAAGTCAAAGGTGGGCAC  
TGGGCATACAACTTCAAGCCAAAGCGAACCAGAAAACATTAACATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT  
GTGCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTTTCCAGCCCAATGATTGTTTACGCGAGAA  
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
TTGGAACTTTGGGATAATGGTGAGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
ACAGAAAATGGCAGATATAGCTTAAAGTTCTGGGCTCATGGAGGAGCAAAACACTGCCAGGCTAAAATTACGGCTCCA  
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATGAAGCAAAACCCGCCAGACCTGAAATTGAT  
GAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAACAGCATCCGGAGGTGCATTGTGGTATCACAAGTCCCAAGC  
CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATTCTT  
ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAGTTCAACGTTATATCATAAGAAATAGTGAAGTATTCTT  
GATCTAAGAGACAGTTTGTATGATGCTCTCAAGTAAATACTACTGATCTGTCAACAAAGGAGGCCAACTCCAAGGAA  
AGCTTTGCAATTTAAACAGAAAATATCTCAGAAGAAAATGCAACCCACATATTATTGCCATTAAAGTATAGATAAA  
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTTATCCCTCAAGCAAAATCCTGATGACATTGAT  
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATTTCTACGCTGGTATTG  
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACATTGAACTTAAACGAAGAAAAAATCTTC  
AAGTAGACCTAGAAGAGAGTTTTTAAAAACAAAACAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT  
GTGTGATCATAAACTCATAAAAATAATTTTAAAGATGTCGGAAGGATGATTTGATTAAATAAAACACTCATGGATA  
TGTA AAAACTGTCAAGATTAAATTTAATAGTTTCATTATTGTTATTTTATTGTAAGAAATAGTGATGAACAAAG  
ATCCTTTTTTCACTGATACCTGGTTGATATTATTTGATGCAACAGTTTTCTGAAATGATATTTCAAATGCAATCAA  
GAAATTAATCATCTATCTGAGTAGTCAAATACAAGTAAAGGAGAGCAATAAACCAACATTGGAAGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
IHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN  
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRNLNR  
MNQAAKHFLQLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
GADSFKNQGVYSRYFTAYTENGRYSLKVRHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPP  
RPEIDEDTQTLEDTSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDN  
FDVGKVQRYIIRISASILDRLDSFDDALQVNTDLSPEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI  
VNFILSTTI

### **Signal peptide:**

amino acids 1-21

### **Putative transmembrane domains:**

amino acids 284-300, 617-633

### **Leucine zipper pattern.**

amino acids 469-491, 476-498

### **N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible][illegible]

## **FIGURE 72**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVKDKRDELVEAIESALETNNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN  
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLFSQY  
NPGIIYGHHDVAPPLQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYR  
KYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 315-319, 324-328

#### **N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

#### **Amidation site.**

amino acids 377-381

[illegible][illegible]

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGTGTC  
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG  
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGA  
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA  
TCCCCAAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG  
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA  
TGTGCAGATGGAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAG  
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGTCAGTGT  
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEK  
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLESQA  
ALAVLGPTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRCLIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 140-163

#### **N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCGAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTCAAGTGGC  
CCCCCGCCTGGTCTCAGTACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA  
TAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC  
CTCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGATTGACCGTCTGGAGTTTGACCTTCTGTGA  
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCC  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT  
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVKEKLTQELKDNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPI SLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNSAASLTMP TLDNIPFSLIVSQDVVKA AVAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLT KDALVLT PASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAGTGTGACATCTATAGC  
ACCTTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGGCCTCCTGGGATTC  
ATTCTGTTCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCAGTGGTGCCTGACAG  
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACGATGCCTAC  
CAAGCCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC  
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA  
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA  
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCACTCTTGTTATGACTCCACAGTGTCCA  
GACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

## **FIGURE 8o**

MASLGLQLVG YILG LLLG LTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNHLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC  
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTCT  
GCCCACGCTGCTTCTGCCCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCGACTCCGCTCCCGG  
ACCAGCGCCTGACCCTGGGGAAGGATGTTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCCTTTT  
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGAGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCAACCAGTGTGTCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGAACCAGGCTGCCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
AGAGGGCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG  
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTTCTAGCCAGACCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTY  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPARRSLERLPSPDGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC  
 GTGGCTTCCGCACCTTAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA  
 TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
 TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG  
 GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG  
 CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC  
 AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCCGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT  
 GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
 ACAGGTGTGACACTGGGCTCAGTTCCCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
 TCTGTCTAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTGTGCC  
 ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
 CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
 GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
 TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACGGACTG  
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
 AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATAGAAAAGCTCCCCAGGAGGTG  
 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA  
 CTGGGAGGTGGACGGAGGACACAATAAAAGTGGCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGA  
 AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCCCTCAGACTGAATGGAGAACATTTGTATTTC  
 ACATTAAATCCCCGTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTTGACTA  
 TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTG  
 AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC  
 CCAGTCAACCAGGAATCAGAGAAAGAGGCCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG  
 TGAGTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCACAT  
 TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
 GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
 CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG  
 AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
 ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEALRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT  
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPLPRGEM

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domain:**

amino acids 239-255



## FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACAATGCTGCTGCTGCTGCTGCCCCCT  
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT  
TACCCCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA  
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCCCCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTATCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAAGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCCTCAGAAGTTGACCATGACTGTCTTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT  
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCTCTTCTGTTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTT  
AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG  
CTTCTGCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAATAATAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAGACACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC  
TCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTSLTQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE  
DANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGEGELQYASLSFQMKPWDSRGQEATDTE  
YSEIKIHR

### **Signal peptide:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCAATTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGGCGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTACCCCTAT  
GGCCAGCGGGAATTCAC TGCGGGATTTGTT CAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTIVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSEPMQHWNRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVIIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCTCCGAGGGGCCATGGGCCGGGTCTCAGGGCTTGCGCCCTCTCGCTTCCTGACG  
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGGTGGCCGCGCTCT  
CTGTCACCCCTGGGCCTCTTTCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTCGAGCGTTGGGAGTGCACACTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCTTCCAGCTG  
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTCATTACCTTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA  
TTAAGACTTATATACAGTTTtaggggacaattAAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCGAACCACAGCCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
AGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTAC  
CATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
TGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGGCAGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTGCTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTTCCAAAATTCCTCTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCCTCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGCGCAGAGCATGTGCTGGATCTGTTT  
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71



## FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT  
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTGGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCAT  
GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRSLKCLLCQDNFLLYNQRSR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

#### **Glycosaminoglycan attachment site.**

amino acids 120-123

#### **Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTTACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAACTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTTGTCACACAACCTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG  
GAACCCAGCAGGCCGCCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAACATATTTGGAAAACCTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG  
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGGCCAGCCTGC  
AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC  
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGGCCCTGGACCGAGAGGA  
GCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC  
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC  
AGAGCTCGGCTGAGCCGGGTACCAGGCTGGCATCCCTTCCTCTTCCTTGAGGCTTCAGACCG  
GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC  
CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAACTCTCCATCATAGAGAGACCTGGGTGT  
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACCACATGGCCCCAGGTA  
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAA  
TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG  
ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
CAGTCCACCAGGTACTGAAGTACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA  
ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGTGTGAAG  
TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGGCCT  
ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA  
CCTCGAGCCCCGCTTCCGCCTCATGGATTTTGGCATTGAGAGGGGAGACACAGAAGGGACTTTTG  
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC  
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCAAGTTGG  
ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTTCCTGTGACCATC  
CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
CTGCATTGAGAAATTTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
ACACCTACACGGTGCTTGTGGAGGCCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA  
TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT  
GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC  
GCCTCCAGACTCTCAATGGTTCCTATGCCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT  
GAACACATAATCCCGTGGTGGTGCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGT  
CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA  
CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCCTC  
ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT  
GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG  
TCCCTTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA  
TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT  
TATGGACTGCCCATGGGAGTGTCCAAATGTGAGGGTGTTCGCCAATAATAAAGCCCCAGAGAA  
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPI SAPAGSFLLT  
IQPSDPI SRLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRQLTLNGSHAYLT LALHWVEP  
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCAACCACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGTGGCACAGCCACCAACTCTGAGTCCAGCACAGACCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC  
AGTGGGGCCAAACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGGCAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTGTGGCGGGCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG  
GTGGAGTCTTAAGTGGTTCGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCTTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCAAGACCTGGTTTCTTTTCTTTCATCCAGGAGACCCTCCAGCTTTGTTTGAGATCCTGAA  
AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTCTGAGATGAAGTCAAGTTATAGGAGAAAACCTCCATGTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVSSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSTTSSGASTATNESSTPSS  
GASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNESRTTSNGAGTATNES  
STTSSGASTATNSDSSTVSSGASTATNESSTTSSGASTATNESSTTSSGASTATNSDSSTTSS  
GAGTATNESSTVSSGISTVTNSESSTPSSGANTATNESSTTSSGANTATNESSTVSSGASTA  
TNSESSTTSSGVSTATNESSTTSSGASTATNSDSSTTSSEASTATNESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFRRPVSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532



## FIGURE 101

GGCCGGACGCCCTCCGCGTTACGGGATGAATTAACGGCGGGTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG  
GGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCAATTCAGGGGAAGGGAATTTGTGGTGCTTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTGTCATGGAAAGGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATTT  
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAAGT  
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTCAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG  
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCTTCCACCTTGCAAGTCTGAACTCAGGGTC  
CTTGTGGTCAAATTGCTCTTATACTGTATTGGACCCTGTTTCAAGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG  
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACT  
GCCATCATTATTTGTTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
TTTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFQIMVSWKGIYFILTLFWGSFFGSI FMLSP  
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCMLRYSYLRLKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLI FPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDI T'VA  
YPHNIPQSEKHLQGDFFPREIH FHVHRYPIDTLPTS KEDLQLWCHKRWEEKEERLRSFYQGEKNF  
YFTGQSVIPPCKSELRLVLVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIEI LACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA  
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATCGGCCTGTATGGGTGCTGGTTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCTGGCTTCTA  
TTTTACTCGGGTACTCTGTGGTGCCCTGTGTGGTGTGTGCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG  
TTTCTGATCTGAAAACGTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACA  
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT  
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT  
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTCAGTTTGAAGGCTTGGTGGAGCCCTATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC  
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTGCTAGTCACGG  
ACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT  
TGCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATCTATAAGCCAGCAT  
TACCTGATACCAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC  
CTCATTAACACAGACACAAAAATCTAAATAAAATTTAACAAATTAACTAAACAATATATTTA  
AAGATGATATATACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAAATATTTAAAT  
ATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 105

CC TTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA  
CTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC  
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA  
ACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAGAACTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
TTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
ATAAACCTTCGAAAATGAAACGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA  
TGACTATGATATTTCTCTTGACAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT  
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT  
GATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
GCCAGGGTGA CTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCAAGCCTGGTGTCTTACTAGAGTTACGGCCTTGC GGACTG  
GATTACTTCAAAAAGCTGATCTAAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG  
GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA  
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTTCATTTGTTCTCTAGAAGTTTGTGAGAATTTGACTTGTGACATAAATTTGTAAT  
GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCCTCAGCTCCTCTCATTTTCAGCAAATATCCATTT  
TCAAGGTGCAGAACAGGAGTGAAGAAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA  
AAGTATTAGGTGTTTTTCTTAGTGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTTCATTTCCAAACAATACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT  
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATATTTATTTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

### **Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCGCGGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGC  
GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
ACGGGGCTCACAATGGCCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA  
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCCT  
GTGGTTCATCCGGTCATGATTGCTGTTTGTGCTGTTTCCCTTATCATTGTGGGGATGTAGGATATTG  
TGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGTCTTGTCATTTTCT  
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCAGTACAATGGTCA  
GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGGAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTAGAGAATTCCAGGATGTTCCAAA  
CAGGCCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCCTT  
TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
ACAGACCAATGATGTCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACT  
TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA  
TAACACCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA  
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAA  
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT  
ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACCTAAAAGAGCAAGCTAACACAT  
TGCTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
ATTTTATAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAAC  
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC  
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA  
AAGGACTTGTATGCTGTTTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTTAAAAA  
GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTACAGAAAA  
TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT  
CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA  
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTAT  
TTCTCAGAATATGGAAAGAAAATTAATAATGTGTCAATAAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTILTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSPLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREP GTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT  
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTCAACCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACAGTTGGATGAGTCTCAAGTCCCTCTATGTGACAACCATGTGAATGGGGAG  
TGGTACCCTTACGGGCATGGCGGGAGATGCCATGCCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGTCAATGGCAGCCACCCCTAGAAAGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAGTCAAGGCTTGGCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCCAGCAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGCACATGCCCTCCAGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
ATGAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT  
GAGTGTGGGGTGGCCGTGTGCTAAGAAGTGTGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCTGGTGTGT  
CTGAGGATAACCACTTGGCAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCTGGAGCTCTTCTGACCAACACCTCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
ACCTGCCAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT  
CATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTTCAAGTTTGTGGGCAAGACCACAAGGAAGTGTCTGCACTGCCGGGTTCTTGTCTGTGGAGTG  
TTGGACGAGCGTTCCCGCTGTGCCAGGTTGCCACGGCGAATGCGTCGTGGGGCAGGAGGAGGACTCAGC  
CGGTCTACAGGGCCAGACGCTAACAGCGGCCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCACCGCCCTCTAAGAACATCTGCCAACAGC  
TGGGTTTCAGACTTCACACTGTGAGTTCAGACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAAGTGTCCA  
CCGAGAAAGACACTCACCCATTTCCTCTATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA  
TTATAGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV  
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNIIPRELVGG  
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLKRLDSLYFGIEPVVHV  
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDKHKEVFLHCRV  
LVCVGLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIDWED

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### **Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

#### **N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

#### **ZP domain proteins.**

amino acids 431-457

#### **Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
CCTGCTGCCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGT  
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGCCAGTCCGCTCTCCAAGGACCGATCCCACTGCAGGTGCTGGACTCGGCCAC  
AGGGAAGTGGTTCTCTGCTGTTTCGACAACCTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCCTGTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGCTGTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA  
GCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG  
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGTGTCAGGCGTCAGTCCAGCTCATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
CTGCGGGGGCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTGCAGTGTGGGAGCCGCTTCCTTCTGCTGCCCTGCCACCT  
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCAT  
TTCTTGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC  
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLOASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSSGGLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC  
TGTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG  
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGGTAGCTGCGGCTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGAACAAGCCGAAGATTTTCATAGGCGATGGCTCCCACTGCCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGGCCAGGACGGGCCGTGGACACCTGTCTCA  
GAAGCAGTGGGTGAGACATCAGCTGCCCCGCCATCTAACCTTTTCATGTCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG  
GAGGTGTTGGGTATCACAAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTTGGCCAGGAGGTGAGCAAGGCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTGAAACCCCAAATCCA  
AACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT  
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTGAGGTTCAAGACCAGCCTGGCCAAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA  
TGTTTATTGTAA

**FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFGQGPCPGRRRD

Signal peptide:  
amino acids 1-15

## FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAACTTCCAATAAATGACTATACTGAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAAC TGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWVARMLGRV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-40

#### **Transmembrane domain:**

amino acids 25-47 (type II)

#### **N-glycosylation sites.**

amino acids 94-97, 180-183

#### **Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

#### **N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 315-317

#### **Cytochrome c family heme-binding site signature.**

amino acids 9-14



## FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC  
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTCT  
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
GATGGTGCAGACTGTTTCCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGGGCTGGGTGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTTCTTATCATGCCCTCAGGCCACAGTGTGCTTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCCGACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA  
CCCAAAAACAAGGAGATCCCCTAGATTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
CGATTTCTCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
TTCTCCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAACTTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT  
ACACTGTGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG  
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTTCTGT  
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCTAAATATAGTTAA  
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC  
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAAGT  
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATAACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAAGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAAACTAATTCCTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY  
V

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG  
GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
CATCACGGGCATGGTGGTGCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
CTGGTGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTACTGTTCTTAACTGCCT  
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACGAGAATGAGATA  
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
CTCTTTTTATCATTTACTTCAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGAACATTTATATCTCACATAGAGACATGCTTATATGGT  
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
CTTGTGTATTAAATTAACATTTTTAAAACGCAGATATTTGTCAAGGGGCTTGCATTCAAAC TGCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
AAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA  
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTCCTTCTTGTA  
CCATTTCTGTTTAGTTTTACTAAAACTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAA  
ACTGACAATCCAATTTGAAAGTTTGTGTGCGCTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTTATATTAATAAATTGTACATTTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK  
IYDSSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVLVLPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG  
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGCAGCC  
GGGAGCCATGCACCCAGGGCCCCGCCGCTCCCCGAGCGGCTCCGCGGCCTCTGCTGCTCC  
TGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGCGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCCTGGACACCCAACTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATAAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGTTGATTTTACACTGTTTTTAAATCTAGCATTATTCATTTTG  
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTA  
AAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAQVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAIYLDQGSPEMNSTINIHRIS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
CTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTTA  
ACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATTTATTTGTTCTTGGAG  
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGGTCCAATTTT  
TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGACAGGGGGCTGTCATGCAACTG  
GCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGTATATTGTGA  
ATCTCAGAAAATTACAGGAGATACCCTCAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
ATAACAGCCTTCAAAAACCTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA  
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATT  
TACGGAACCTTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCGCAACCTGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
TCTTTGCTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC  
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGT  
CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA  
TCGAAGCTTTTCAGTGACCCAGTGTTTTCCAGTGCTGCCGAATCTGCAGCGCCTCAACCTGGAT  
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTT  
TTAAAGGTCTAAGGGAGAAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
GGCTCTCCCAAAGCCGACGTTTAAAGCCAAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTT  
TGCCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTGCTGGTTAT  
CTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
GGCACAGGAAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTA  
GATTATAAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGCT  
GGGAAATAAGTGGTGCTTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC  
TTCCCTCTCCCTCTCACTTTGGTGGAAGATCCTTCCCTGTCCGTTTTAGTGCATTTCATAATACT  
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
GAACTCCGGTTTAAATAATACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCGATTT  
GTTTTAAGATAAAACTCTTTTCATAGGTAAAAA

## **FIGURE 124**

MGENVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLLSLHLRSNSLRTPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLEHNQFSKLNLFRLVSLQNLQWNKISVIGQTMSTWSSSLQRLDL  
SGNEIEAFSGPSVVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512



## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTTGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATTCGGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC  
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSRIMNQP  
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCCAAGCAGGTGCGCGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGCGGCCATGCCAGGCCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCCTACAGATGTGACCTAT  
CAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA  
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT  
GAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG  
AGACACAATTGCGCTTCAAACCTCCAGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCTTCATGGCTTGCTCTGCTCTGGATTTTAGGTGTTGATTTCTGGAT  
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTTGAGATTTTATA  
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTTACTTGTAACTTGTTCCTGTGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG  
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCTCCTGCGCTGCCCCACTGCACCCTCTCCCCCTATCTATCTCCTTCTCGGCTCCCC  
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCCAGTGGATTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAA  
AAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTTGCCCGGAGC  
ACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAAATCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA  
GGATGGAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA  
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTGGGAACCTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAAATGACAGGATTCGTTCTTAATTTCAATTAATAAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGGHTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

## FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCTTCAGAT  
TTGAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTTACCAACCT  
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTGTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCTTGGGGTTT  
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG  
GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGGGAATTCCCTGACTGCTGCACCAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCCAATGCTTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTCTGTTGGGATGGCTATTAAAGGATCTCAATGCAGAACCTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
CAATTACAATTACTGTGAAGTCTGTACACCTCTGATACCATTCAATCTCTTGGAACTTGCTCTACCTATG  
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC  
CCATGGAACCAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG  
TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT  
AAGCAATGAACCCATCTCGAAGGAGGAGTTGTAAATACACACCATATTTCTCTCTAATGGAATGAATCTGT  
ACAAAAACAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIR TITYDSLSKIPYL  
EELHLDDNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLT AAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNLSNLPQGIFDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRK TITITVKS VTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVCMPMETS NLYLFD ETPVCIETETAPLRMYNPTTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYS KGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSESSSNRSYRDSGIPDS DSHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44



## FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA  
GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
GGCGTGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCAGGAGCCCCGTC  
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG  
GTTTGGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCTCTGGGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCTACCCACCGGGACATCTTCATGGAAAACATCATGTTCTG  
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC  
AATTCCTTGCCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT  
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGS LGLARAQGAERTVSSEQRPAMASLG LLLLLLLLTALPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRLVEEQ LKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQ RSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSS EPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQG PLQQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCMGGFSDFYKLRWLEAILS WQKQEGCGFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCLILP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRD PPTSGSQSVGL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 39-56

#### **Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

#### **N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

#### **Amidation site.**

amino acids 10-14

#### **Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCTTAAAG  
ACAGATGGGAGTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCCTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGACAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGGAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT  
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
RVLVDGEEHVGLKTDGFSFVVDIPSGSYVVEVVSAPAYRFDVVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPPLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

### **Important features of the protein:**

#### **Signal sequence:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 161-182

#### **N-glycosylation site.**

amino acids 184-187

#### **Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

#### **N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

#### **Amidation site.**

amino acids 238-241

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAACAA  
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCAGGC  
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTCACGGGAGGCTTGGCAGT  
TTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGTCTTGCCCTCAGC  
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGGAAC TAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA  
ACCACCATCTCTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
CTTCCTTGATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT  
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA  
ATGTATTTATTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATTC TAGAAGAGTG  
CTAGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGATGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG  
CCAGGAATCTACACGGCCAGCATGTATTCTACAAATAAAGTTTCTTTGCATACCAAAAAAA  
AAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLT IKDLRLSHAHTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

## FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCCGGTTCGCATCCAGCC  
 TAGCGTGTCCACGATCGCGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
 TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA  
 CACGGAGCGGAGCCCCAGCGCCGAACCCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
 ACCACCTCTCTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG  
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAAAAAGGAGCATCTCACAGT  
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
 CCTTCTCGGCTTTGTGCGACGTCATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGA  
 TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA  
 TTCCCAAAGCATTGTTGGGAATATGATGGAAACAACCTCATTTTTCGTGTGAGATTACACAGAGGT  
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC  
 TCCACTACCTGGGCTGGACCACATTGGCCACATTTACAGGGCCCAACAGCCCCCTGATTGGGCAG  
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA  
 GACGCCTTTACCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
 GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAA  
 CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGGAAGGAAGAC  
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG  
 AATGTGCCGTATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG  
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAGTCTTATTCAACCTGGGCTCCAAGG  
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGACAAAGTGGCCAG  
 TTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
 CTGTCATCTCCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTCGGCCGTTACGT  
 CATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT  
 GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCTGGAC  
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCAGACAGGTG  
 TTCACATCTGTGCTGTGAGGTGAGATGCCTCAGTTCTTGGAAGCTAGGTTCTGCGACTGTTAC  
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
 TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
 CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAAGATGCATCCT  
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTGGAAATCTTAGTCCTTGGCC  
 TCGGACACCTTCATTGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC  
 ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
 ACCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGCCCTGTGCTGAGTGT  
 CTGACCGAGACACTCACAGCTTTGTGATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG  
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG  
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHAEPPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSEVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208



## **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT  
TCCCTATAGAAAACAACCTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACCTACATACGCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT  
GGCTGCCCCAAAAGGAATCAGCACGCCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTGAGCGATTAGGAACTGCCCCATTGAACGCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAAACCAAACCTGCTCACT

## **FIGURE 142**

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPTI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

## FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCTTCCCTGTCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAATCTCAGATCAGTGTTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

## FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCCATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGACTGCCCAGATCA  
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCAACATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACCTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHKRKNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT  
CCTGATGATTTATAGACTCAAAGAAAACATGTTCAGAAGCTCTCTTCTTCTGGCCTCCTCT  
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTGAAATTT  
CAACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68



## FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCCAGTCC  
CGGCCCCCTCTCCGCCCCACCCACCCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTCTATA  
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGAAGAAATGGGGTT  
CCTCGGGACCGGCACTTGATTCTGGTGTAGTGTCCCGATTCAAGCTTTCCCCAAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAAGACCTTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGAAGATGTTGATTCAACCAAGAATCGAAAACCTG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG  
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTGAGGAACCTCA  
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAACAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT  
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
CAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAAACACTTCTAATTCTGTGATTAAAAATTTTGGACCAAGG  
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIAKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA  
GATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGGTGGCTGGATGCCAGCTGTCCCCGTATCCTGGGTGTCCAGGGTGGAAAG  
CCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGGCTCACC  
TCCAGCTTCGAGTGGCTGCCTACCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTGAGACTCAGCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAAGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTTTGTCTTCTGGTTCCAGTTTGGATAAAATCTGAGATTTGGAGCTCAGT  
CCACGGTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTAAAAACCATGTGGGGTAA  
CTGGGAATAACATGAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCT  
TAATGGTAACGACAAGTGTACCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA  
GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA  
TGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGTCAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA  
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTAATTAAGATACCTATTTATATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT  
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTCTACAATGAAGATGA  
ATTCTTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
TTGTCTCAGCCTCCACTTCCCGAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAATAATCATCTGGTAATTCTTCTCTAGAAG  
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG  
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT  
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGAAGAGGCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTCGGCTGTTTTAA  
GCCACCAAGGATAAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT  
CTCCTCGTGTTTACATTCTGTGTGTGTCCTTCCACAAATGTACCAAAGTTGTCTTTGTGACCAA  
TAGAATATGGCAGAAGTGTGGCATGCCACTTCCAAGATTAGGTATATAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
GCCCCAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGG  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGWGNAPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCTGCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTC  
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT  
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGATATCCC

## **FIGURE 154**

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCAGTGCAGAGGGC  
TGCCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT  
TGCCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCCTGTGAAGTGTCTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCTCTCTCAGGAAAGGTTTTCAAA  
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG  
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
TGTTTGTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTATTGAATGTATAGAGATTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTYSHWPSCCPKQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHTKGYCLERRLYRVS LACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156



## FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTTCAATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA  
GTAGAAGTGAAGTTTACAACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGAAGTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCAGAGTGAAGTGCATCCTTGAAA  
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLDLRLRVEPVTTSVATGDYSILMNVSWV  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQVVSAGKRSQACHD  
GCCSL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **Transmembrane domain:**

amino acids 290-309

#### **N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

#### **Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

#### **N-myristoylation site.**

amino acids 116-122

#### **Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA  
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

### **Signal sequence:**

amino acids 1-30

### **N-glycosylation site.**

amino acids 83-87

### **N-myristoylation sites.**

amino acids 106-111, 136-141

## FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCT  
TGGCACTGGGCCGAAGCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT  
CGTGCTGTCTCCGGGCCCCGTGCTGGCGCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA  
TGCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCCTACCTACTGCCCGCTGCGTCTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGAGTGAGGTACGAATCTGGTCTCTACTCAGCCAGGTACGAGAA  
GGAACCAACACACACAGCAGCTGCCCTGCCCTGGCTCAACGTGTGACGAGATGGTGACA  
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAACCCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA  
CCACACAGACCTGGTTCCCTGCCTCTGTATTAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTCAGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCGGACTG  
CGACTGCTGACCTGCAGAGCTGGCTGTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT  
GTCTGGCGGGCTCCGGGTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCTGGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTCAGGTG  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCTCTCAAAGA  
CGATGTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCTTGAACCCA  
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCTGCTACTCTTTGCCG  
CTGCGCTTTCCCTCATCTCTCTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAA  
CAGGACGTCCGCTCGGGGGCGGCCGAGGGGCCGCGGCTCTGCTCTTCTCTCCCGGTGCGGTGGCGCT  
CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTCCGGCCTGTGCCAGCTGCCGCTGCGCGTGG  
CCGTAGACCTGTGGAGCCGTGTAAGTGAAGCGCGCAGGGGCCCGTGGCTTGGTTTACCGCGCAG  
CGGCGCCAGACCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTTCTCTCCCGGTGCGGTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGCGCACGGCCCGCACGACGCTTCC  
GCGCTCGCTCAGCTGCGTGTGCCCCGACTTCTTGAGGGCCGGGCGCCCGGCAGCTACGTGGGG  
GCCTGCTTCGACAGGCTGTCCACCCGGACCGGTACCCGCCCTTTCCGCACCGTGGCGTCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCTTCCG  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACGCCAGCCCTGGATAGCTACTTC  
CATCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTCTAAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPLGLSCRLWDSIDLCLPGDIVPAPGPVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV  
QVPAALVQFGQSVGSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVVSADGDNVHLVLNV  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN  
LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG  
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP  
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT  
LPSQLPDLFGALQQPRAPRSGRLQERAEQVSRLQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain.**

amino acids 453-475

### **N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

### **Glycosaminoglycan attachment site.**

amino acids 583-586

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

### **N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT  
GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA  
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTACGCGGATCACCCGGAAGTCTGC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
GTCAGTGGGGAGGCGGTGAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAGACATCTTCCATGACCTG  
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAATGCACCTTGGAGGGAAGCAGAGAGA  
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA  
CCTGGGCCAAGGAGAGTCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
TACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCGTCGCAGTACTCTGCTACCTGAG  
CTACAGATATGTACCAAGCGCCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT  
TCCAGCGCTGCGCTTCATCCAGGAGCAGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
AGTCTGGCCCAGCCTGTCCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCCTATGCCCCAAACGCTGCCCTGAG  
GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTCTACGCCCCACA  
GGCCATCTCTAAGGTCCAGCCTTCTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTCTAAA  
CACCTTAGGCCTAAAGGTGAGCTTCTAGAAAGAGCCACCAGCTGGAAGTGCATGTTAGGTGGCCT  
TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCAACCAGC  
CCCTGGGGATTGTCACAGACAGAATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA  
CCACAGTACCTAAAGGGCCAGTCCCCCTCTCTCAGTCCAGATCGAGGGCCACCCCATGTC  
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
GAGCAGCCACAGAACTGGATTCTTTTTAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCCCTG  
AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA  
ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA  
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG  
CAAGGCAGAAATGACAGTGAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCTTGGCCCATCTCTGGCCAGTTTC  
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTATTGTTCAAAGGTGGGAAGAGA  
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGTGGGCAGAACCAAGAACCTGC  
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA  
TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCATTCTCTGATAGAACAAGC  
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT  
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
TGTAATGATGTACAACCTTTGCAAGCTCTGCCTTGGGTTAGCCCATCTGGGCTCAAATTCAGC  
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCCTC  
ATCTGTAATGTGGGGATCATAACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAACGGTAGCTATTTAAAAA  
AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTELYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLDPRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFPYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSIAM  
EESQEAKSLHQPLGICTDRSTDPNVLHSGEETPQYILKGQLPLLSSVQIEGHFMSLPLQPPSGPC  
SPSDQGPPSPWGLLESVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

### **Signal sequence.**

amino acids 1-17

### **Transmembrane domain.**

amino acids 233-250

### **N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

### **N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570



## FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA  
AGTGTGGAACACAGTTTTTGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAAGTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGC GTTATT  
CATTACAGCAAAGGATTTTCGTTGGCATCAAATCTAAGTTTGTTTTACAAAGATTGTTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCAATTTTGTAGCCAAACAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEECMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDVPVEPEAFRAEDGEDGA  
FSESTEGLQGQPSAQESHPTHSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGAAGAGAAGCAAAGCGC  
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCTAACTTC  
 AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG  
 CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCGGGCAGCTGGGCTCGGGC  
 GGCAGAGTGTAGGGCCCGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
 GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG  
 TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTGCAGC  
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAGT  
 GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCCTCA  
 GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
 ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG  
 TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATTCCCAGTACCGAAACTGGTACACAG  
 ATGAACCTTCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGC  
 CTTGGGGGTCCCTACCTTTACCAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
 CAAGTATGAACCAGAGATTAATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG  
 GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCAATCTAATTTATGTTGTT  
 ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT  
 GCATAAAAGTAAAGGAAGAACAATACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA  
 CCAGAAAAGAAAGTGGCATGGAAGTATAATACTCATTGACTTGGTTCCAGAATTTTGTAATCT  
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC  
 AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTCA  
 TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA  
 ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA  
 TGTGTGTTAGAAAGCAATTCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAA  
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA  
 ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAG  
 AAACCTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT  
 TTTCTCGAAATAATTCATCTTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA  
 AATAAGAAGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT  
 TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAATTAACAGATT  
 TTGTAATAATGTAACCTTGTGTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG  
 TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
 GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG  
 ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTCCCTAGCTGTATTTAGCCTCTG  
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAAATGGGTTGG  
 AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGTCTGAGATAGAAAATGGTGGCTCCTTT  
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTTCTCAAGAGAAAGTTGTAAGTCT  
 CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTCTGGGGGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFRRVSVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNKYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217